

Amendments to the Claims

Please cancel claims 14 to 22, 27 to 35, 39 to 43, 45 to 47 and 49 to 77 without prejudice.

Upon entry of the present amendment, the status of the claims will be as follows:

1. (Original) A method to determine gender of a canine subject, comprising contacting a nucleic acid sample from the canine subject with at least one probe or primer specific for a canine amelogenin gene, and using the binding of the at least one probe or primer to detect a difference between the canine amelogenin gene on the Y chromosome and the canine amelogenin gene on the X chromosome, thereby determining gender of the canine subject.

2. (Original) The method of claim 1, wherein gender of the canine subject is determined by contacting the nucleic acid sample with at least one probe or primer that specifically binds SEQ ID NO:22 and/or SEQ ID NO:23.

3. (Original) The method of claim 1, wherein gender of the canine subject is determined by contacting the nucleic acid sample with at least one probe or primer that specifically binds SEQ ID NO:10 and/or SEQ ID NO:11.

4. (Original) The method of claim 3, wherein gender of the canine subject is determined by contacting the nucleic acid sample with a primer pair, wherein a first primer of the primer pair specifically binds to SEQ ID NO:6 and/or SEQ ID NO:7 and a second primer of the primer pair specifically binds to SEQ ID NO:8 and/or SEQ ID NO:9.

5. (Original) The method of claim 4, wherein the first primer comprises at least 10 nucleotides of SEQ ID NO:3 and the second primer comprises at least 10 nucleotides of SEQ ID NO:5.

6. (Original) The method of claim 5, wherein the first primer is SEQ ID NO:3 and the second primer is SEQ ID NO:5.

7. (Original) The method of claim 5, wherein the first primer is SEQ ID NO:4 and the second primer is SEQ ID NO:5.

8. (Original) The method of claim 5, wherein the primer pair generates an amplification product that is a different length for the amelogenin gene on the X chromosome and the amelogenin gene on the Y chromosome.

9. (Original) A method to determine gender of a canine subject, comprising contacting a nucleic acid sample from the canine subject with at least one probe or primer specific for canine amelogenin, and detecting binding of the at least one probe or primer, thereby determining gender of the canine subject.

10. (Original) The method of claim 9, wherein gender of the canine subject is determined by contacting the nucleic acid sample with at least one probe or primer that specifically binds SEQ ID NO:22 and/or SEQ ID NO:23.

11. (Original) The method of claim 9, wherein gender of the canine subject is determined by contacting the nucleic acid sample with at least one probe or primer that specifically binds SEQ ID NO:10 and/or SEQ ID NO:11.

12. (Original) The method of claim 11, wherein gender of the canine subject is determined by contacting the nucleic acid sample with a primer pair, wherein a first primer of the

primer pair specifically binds to SEQ ID NO:6 and/or SEQ ID NO:7 and a second primer of the primer pair specifically binds to SEQ ID NO:8 and/or SEQ ID NO:9.

13. (Original) The method of claim 9, wherein binding of the at least one probe or primer distinguishes the canine amelogenin gene on the X chromosome from the amelogenin gene on the Y chromosome.

Claims 14-22 (Cancelled)

23. (Original) A method to detect binding of at least one primer or probe to a canine amelogenin gene, comprising contacting a nucleic acid sample from a canine subject with at least one probe or primer specific for canine amelogenin.

24. (Original) The method of claim 23, wherein the nucleic acid sample is contacted with at least one probe or primer that specifically binds SEQ ID NO:22 and/or SEQ ID NO:23.

25. (Original) The method of claim 23, wherein the nucleic acid sample is contacted with at least one probe or primer that specifically binds SEQ ID NO:10 and/or SEQ ID NO:11.

26. (Original) The method of claim 25, wherein the nucleic acid sample is contacted with a primer pair, wherein a first primer of the primer pair specifically binds to SEQ ID NO:6 and/or SEQ ID NO:7 and a second primer of the primer pair specifically binds to SEQ ID NO:8 and/or SEQ ID NO:9.

Claims 27-35 (Cancelled)

36. (Original) A method to genotype a canine subject, comprising contacting a nucleic acid sample from the canine subject with at least one probe or primer specific for canine amelogenin, and detecting binding of the at least one probe or primer, thereby genotyping the canine subject.

37. (Original) The method of claim 36, wherein the nucleic acid sample is contacted with at least one probe or primer that specifically binds SEQ ID NO:22 and/or SEQ ID NO:23.

38. (Original) The method of claim 36, wherein the nucleic acid sample is contacted with at least one probe or primer that specifically binds SEQ ID NO:10 and/or SEQ ID NO:11.

Claims 39-43 (Cancelled)

44. (Original) The method of claim 36, further comprising genotyping the canine subject at a microsatellite locus.

Claims 45-47 (Cancelled)

48. (Original) The method of claim 44, wherein the microsatellite locus is at least one of PEZ1/CATA1, PEZ3, PEZ5, PEZ6, PEZ8, PEZ10, PEZ11, PEZ12, PEZ13, PEZ15, PEZ16, PEZ17, PEZ20, PEZ21, FH2010, FH2054, and FH2079.

Claims 49-77 (Cancelled)